

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 18, 2002, 04:47:24 : Search time 145.84 Seconds

(Without alignments)
200.305 Million cell updates/sec

Title: US-09-719-748-2_COPY_13_275

Perfect score: 1343

Sequence: 1 YDIGELSGQFAIVKRCRE.....LVKTRKRLTIQELRHPWI 263

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.GeneSeq_032802.*

1:	/net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2:	/net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
3:	/net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
4:	/net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
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6:	/net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
7:	/net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
8:	/net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
9:	/net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
10:	/net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
11:	/net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
12:	/net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
13:	/net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
14:	/net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
15:	/net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
16:	/net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
17:	/net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
18:	/net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
19:	/net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20:	/net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
21:	/net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*
22:	/net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1343	100.0	360	21	AAV44674
2	1278	95.2	359	22	ABG09274
3	1121	83.5	454	20	AAV06921
4	1121	83.5	454	22	AAV93338
5	1117	83.2	454	22	AAV94378
6	1117	83.2	454	22	AAV67425
7	1106	82.4	448	20	AAV06922
8	1079	80.3	1423	16	AAV74205
9	1079	80.3	1423	19	AAV71367
10	649	48.3	260	20	AAV43924
11	638	47.5	414	20	AAV27161

12	638	47.5	414	22	AAV65625	Novel protein kina
13	634	47.2	372	22	AAV65624	Novel protein kina
14	627.5	46.7	7107	22	AAV58144	Drosophila melanog
15	625	46.5	372	20	AAV27162	Human DRP2 protei
16	625	46.5	372	22	AAV65623	Human protein kina
17	617.5	46.0	291	22	AAV85502	Human protein kina
18	611.5	45.5	839	21	AAV65684	Human prostate can
19	599.5	44.6	814	22	AAV65654	Human protein kina
20	599.5	44.6	819	20	AAV42111	Human ischaemic he
21	596.5	44.4	413	22	AAV65652	Novel protein kina
22	574	42.7	913	22	AAV62810	Drosophila melanog
23	574	42.7	913	22	AAV65658	Drosophila melanog
24	574	42.7	1289	20	AAV27163	Peptide Seq ID NO:
25	574	42.7	1289	21	AAV56781	Human Trid protein
26	571.5	42.6	261	20	AAV43923	Rabbit Trid protein
27	569.5	42.4	612	22	AAV03521	Human protein kina
28	559.5	41.7	536	22	AAV67344	Amino acid sequenc
29	553	41.2	307	22	ABG08502	Novel human diagn
30	542.5	40.4	307	18	AAV43892	Novel human phosph
31	542.5	40.4	307	20	AAV76803	Human phosphorilas
32	542.5	40.4	307	21	AAV52303	Novel human phosph
33	541	40.3	26926	22	AAV05396	Human titin (conn
34	525	39.1	638	22	ABV58483	Drosophila melanog
35	514	38.3	355	22	AAE11777	Human kinase (PKIN
36	514	38.3	355	22	AAV41268	Human polyphosph
37	514	38.3	355	22	AAV50055	Human kinase (PKIN
38	514	38.3	356	22	AAV84360	Murine dendritic C
39	514	38.3	357	22	AAE11768	Amino acid sequenc
40	514	38.3	357	22	AAV03508	Human kinase (PKIN
41	514	38.3	385	22	AAV39482	Human polyphosph
42	514	38.3	385	22	AAV84359	Amino acid sequenc
43	508	37.8	493	22	ABV65515	Drosophila melanog
44	508	37.8	493	22	ABV65515	Drosophila melanog
45	508	37.8	493	22	ABV66556	Drosophila melanog

ALIGNMENTS

RESULT 1	AAV44674	standard; Protein: 360 AA.
ID	AAV44674:	
AC	AAV44674:	
XX		
DT	18-APR-2000	(first entry)
XX		
DE	Human DAP-kinase-related protein 1 (DRP-1).	
XX		
KW	DAP-kinase-related protein 1; DRP-1; Death-Associated Protein;	
KW	calmodulin-dependent serine/threonine kinase; apoptosis; dimerisation;	
KW	cytoskeletal; antiproliferic; immunosuppressive; metastasis; tumour; human;	
XX	treatment; cancer; psoriasis; autoimmune disease; screening.	
OS	Homo sapiens.	
XX		
PH		
FT	Key	Location/Qualifiers
FT	Domain	13..275
FT	Domain	/label= Serine/Threonine_kinase_domain
FT	Domain	292..320
FT	Domain	/label= Calmodulin_regulatory_domain
FT	Region	321..360
FT		/label= C-terminal_region
FT		/note= "Critical for DRP-1 dimerisation and apoptotic induction"
XX	WO996030-A1.	
XX	23-DEC-1999.	
XX	15-JUN-1999.	99WO-US13411.
XX	15-JUN-1998.	98US-0089294.

XX (YEDA) YEDA RES & DEV CO LTD.
 PA (MCIN/) MCINNIS P A.
 XX
 XX Kimchi A;
 DR WPI: 2000-147148/13.
 DR N-PSDB; AAZ49765.
 XX
 PT Calmodulin-dependent serine/threonine kinase capable of inducing
 PT apoptosis used in the treatment of e.g. cancer
 XX
 PS Claim 1: Fig 1; 67pp; English.
 XX
 CC The present sequence is DAP (death-associated protein)-kinase-related
 CC protein 1 (DAP-1), which is a calmodulin-dependent serine/threonine
 CC kinase. DAP-1 is a cytoplasmic protein capable of inducing apoptosis
 CC by dimerisation. It shows significant homology to DAP kinase. It has
 CC cytosolic, antiproliferative and immunosuppressive activity and can be
 CC used for inhibiting growth/metastasis of tumours and promoting of cancer,
 CC death of tumour cells. It can also be used in the treatment of cancer,
 CC psoriasis and autoimmune diseases. Fragments of DAP-1 DNA are useful as
 CC probes for screening individuals with a predisposition to cancer.
 XX
 XX Sequence 360 AA:
 SQ
 Query Match 100.0%; Score 1343; DB 21; Length 360;
 Best Local Similarity 100.0%; Pred. No. 1,1e-127; Indels 0; Gaps 0;
 Matches 263; Conservative 0; Mismatches 0;
 QY 1 YDGEELSGSOFATVKKCKREKSTGLEFAKFKKRSRGRVSRREIEREYSILROYL 60
 DB 13 YdGeeLsgsfatvkkckreksGLEFAKFKKRSRGRVSRREIEREYSILROYL 72
 QY 61 HHNYITLHDVYENTDVVHLELVSGGELFDFLAQKESLSEEAATSFIKQILDGVNLT 120
 DB 73 hhnvltldvyentdvvhllslvsgelfdflaqkeslseeaatsfikqildgvnylht 132
 QY 121 KKIHFDLKPEINMLDKNIPRIPIKILDFGLAHEIDGVEFNIFGTPFEVAPETVNE 180
 DB 133 kkihfdlkipenimldknipriphikildfglaneidgvefnifgtpfevapevny 192
 QY 181 PLGLEADWMSIGVITYILLSGASPLDPTKQETLANITSVSYDDEPFSHTSELANDFI 240
 DB 193 plgleadwmsigvityillsgasplldptkqetlanitsvsyddefsfhtselakdfi 252
 QY 241 RKLIVKEPRKRLTIOEALRHPWI 263
 DB 253 rklivkeprkrltiqealrhpwi 275
 100

RESULT 2
 ABG09274
 ID ABG09274 standard; Protein: 359 AA.
 XX
 AC ABG09274;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #9265.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX

PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 XX (HYSE-) HYSEO INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI: 2001-639362/73.
 DR N-PSDB; AAS73461.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 XX
 PS Claim 20; SEQ ID NO 39633; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polynucleotide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on human
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 359 AA:
 SQ
 Query Match 95.2%; Score 1278; DB 22; Length 359;
 Best Local Similarity 98.8%; Pred. No. 4,2e-121; Indels 0; Gaps 0;
 Matches 252; Conservative 1; Mismatches 2;
 QY 9 SCGFATVKKCKREKSTGLEFAKFKKRSRGRVSRREIEREYSILROYLHHNYITLH 68
 DB 20 sgGfatvkkckreksGLEFAKFKKRSRGRVSRREIEREYSILROYLHHNYITLH 79
 QY 69 DYVENRTDVVHLELVSGGELFDFLAQKESLSEEAATSFIKQILDGVNLT 128
 DB 80 dyventrdvvhlslvsgelfdflaqkeslseeaatsfikqildgvnylhtkkihfdl 139
 QY 129 KPEINMLDKNIPRIPIKILDFGLAHEIDGVEFNIFGTPFEVAPETVNE 188
 DB 140 kpenimldknipriphikildfglaneidgvefnifgtpfevapevnyelgleadn 199
 QY 189 WSTGVITYILLSGASPLDPTKQETLANITSVSYDDEPFSHTSELANDFI 248
 DB 200 wstgvityillsgasplldptkqetlanitsvsyddefsfhtselakdfiklrvket 259
 QY 249 RKRLTIOEALRHPWI 263
 DB 260 rkrltiqealrhpwi 274

RESULT 3
 AAY06921
 ID AAY06921 standard; Protein: 454 AA.
 XX
 AC AAY06921;
 XX

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DT 01-JUL-1999 (first entry)
XX
DE Human ZIP-kinase (serine/threonine kinase).
XX
KW zipper Interacting Protein Kinase; zip-kinase; serine/threonine kinase;
XX leucine zipper domain; transcription factor Atp4; gene therapy; cancer;
XX human; murine.
XX
XX Homo sapiens.
XX
XX EP911408-A2.
XX
XX 28-APR-1999.
XX
XX 24-SEP-1998; 98EP-0307747.
XX
XX 26-SEP-1997; 97JP-0261589.
XX
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
XX Akira S, Kawai T;
XX
XX WPI: 1999-246420/21.
XX
XX N-PSDB; AAX34656.
XX
XX New Recombinant zipper Interacting Protein Kinase (ZIP-kinase)
XX protein and DNA, useful as anticancer agents
XX
XX Claim 1; Page 15-18; 33pp; English.
XX
XX The invention provides human and murine recombinant zipper Interacting
XX Protein Kinase (ZIP-kinase) proteins. These proteins are serine/threonine
XX kinases which bind the leucine zipper domain of transcription factor
XX Atp4. Host cells containing vectors comprising the ZIP-kinase nucleic
XX acids are used for the recombinant expression of the proteins. ZIP-kinase
XX protein and DNA are useful as gene therapeutic agents against cancer, and
XX as anti-cancer agents. The present sequence represents a human ZIP kinase
XX protein.
XX
XX Sequence 454 AA:
XX
SQ
Query Match 83.5%; Score 1121; DB 20; Length 454;
Best Local Similarity 79.8%; Pred. No. 4.9e-105;
Matches 210; Conservative 36; Mismatches 17; Indels 0; Gaps 0;
OY 1 YDIGEELSGCGAIVKCKCREKSTGLEVYAKFKRKQSRASRGVSRRETEREVSTLROYL 60
DB 13 yemgeelsyggafayrkcrcqkgytgyeaaikfkkrtrissrrrgvsreeeterevnlirelr 72
OY 61 HHNVITLHDVENVRTDVVHILELVSGGELDFDLAOKESLSEEEATSFIKOILDGVNYLHT 120
DB 73 hpnltlthdfenkckdvlllelvsggelfdflaekesltedeatqgflqldgnyhnl 132
OY 121 KKIAMFDLKPKEIMLDKNIPHPHKLDFGLAHEIEDGVEKKNIPTGPEYAPETIVNVE 180
DB 133 krlahfdlkrpeimldknvprkikldfglahklsagneknlifgtpetvapeivnye 192
OY 181 PLGLEADWMSGVITVITLLSGASPLDGRKQKOTLANINVSVDPPDEEFSHNSLAKDRT 240
DB 193 plgleadwmsygvitvillsgasplldgkqetlnlsavnydfdeeyfnsnslakdrt 252
OY 241 RKLAVETRRKRLTIOEALNHPWI 263
DB 253 rlllvkdpkrmtlqsglsnswl 275
RESULT 4
ID AAM93338
XX AAM93338 standard; Protein; 454 AA.
XX
XX AAM93338;
XX

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[illegible]

XX	AAB94378	ID	AAB94378 standard; Protein; 454 AA.
XX	AC		
XX	AAB94378:		
DT	26-JUN-2001	(first entry)	
XX	DE	Human protein sequence SEQ ID NO:14926.	
XX	Human;	primer; detection; diagnosis; antisense therapy; gene therapy.	
OS	Homo sapiens.		
PX	EPI074617-A2.		
PN	07-FEB-2001.		
PD	28-JUL-2000; 2000EP-0116126.		
PF	29-JUL-1999; 99JP-0248036.		
PR	27-AUG-1999; 99JP-0300253.		
PR	11-JAN-2000; 2000JP-0118776.		
PR	02-MAY-2000; 2000JP-0183767.		
PR	09-JUN-2000; 2000JP-0241899.		
PA	(HELI-) HELIX RES INST.		
XX	Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;		
PI	Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;		
XX	WPI: 2001-318749/34.		
DR	Primer sets for synthesizing polynucleotides, particularly the 5602		
PT	full-length cDNAs defined in the specification, and for the detection		
PT	and/or diagnosis of the abnormality of the proteins encoded by the		
PT	full-length cDNAs -		
XX	Claim 8: SEQ ID 14926; 2537bp + CD ROM; English.		
PS	The present invention describes primer sets for synthesizing 5602		
CC	full-length cDNAs defined in the specification. Where a primer set		
CC	comprises: (a) an oligo-dT primer and an oligonucleotide complementary		
CC	to the complementary strand of a polynucleotide which comprises one of		
CC	the 5602 nucleotide sequences defined in the specification, where the		
CC	oligonucleotide comprises at least 15 nucleotides; or (b) a combination		
CC	of an oligonucleotide comprising a sequence complementary to the		
CC	complementary strand of a polynucleotide which comprises a 5'-end		
CC	sequence and an oligonucleotide comprising a sequence complementary to a		
CC	polynucleotide which comprises a 3'-end sequence, where the		
CC	oligonucleotide comprises at least 15 nucleotides and the combination of		
CC	the 5'-end sequence/3'-end sequence is selected from those defined in		
CC	the specification. The primer sets can be used in antisense therapy and		
CC	in gene therapy. The primers are useful for synthesizing polynucleotides,		
CC	particularly full-length cDNAs. The primers are also useful for the		
CC	detection and/or diagnosis of the abnormality of the proteins encoded by		
CC	the full-length cDNAs. The primers allow obtaining of the full-length		
CC	cDNA easily without any specialised methods. AAH03166 to AAH13628 and		
CC	AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to		
CC	AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632		
CC	represent oligonucleotides, all of which are used in the exemplification		
CC	of the present invention.		
XX			
SQ	Sequence	454 AA;	
	Query Match	83.2% Score 1117; DB 22; Length 454;	
	Best Local Similarity	79.5% Pred. No. 1.2e-104;	
	Matches 209; Conservative	36; Mismatches 18; Indels 0; Gaps 0;	
QY	1 YDGEELSGGQFAIVKCKREKSTGLDYAKETIKRKSAPASRGVSRKEIREYSILROYL 60		
	::::::::::::::::::::: ::::::::::::::::::::: :::::::::::::::::::::		
DB	13 ymgdeagsgqdfivkrckrqktgkyekayakfkfkrllssrrgyrsreelervallireir 72		

QY		61	HHNVITLHDVYENRTDVHILLETIVSGGLFPDLAQKESISEEASFLKQLIDGVNYHT	120
Db		73	hpnltlhdifektdvlllelvsgglfdflnaekesltedeaqcqlldgvhyhs	132
QY		121	KKIAHPDLKRENTMLDKNIPRIPIKIDPGLAHEIEDVEERKNIFGPEFYAPEIWTNE	180
Db		133	kriahfdlpkenlmldoknvpnrkrlidglahek.leagnefknlitgpefaveplmye	192
QY		181	PLGLEADWMSIGVITYILLSGASPFGLDTKOEFLANITSYSVPDEFESHSELAKDPT	240
Db		193	pgleadwmsigvityillysgaspfigetketcltnsavnydfdeeyishngelakdft	252
QY		241	RKLKYETRRRLTIOELRHPMI	263
Db		253	rllvkdpkrrmtclagslehswl	275
RESULT	6			
ID	AAG67425	standard; Protein:	454 AA.	
AC	AAG67425;			
DT	26-NOV-2001	(first entry)		
DE	Amino acid sequence of a human protein kinase/protein phosphatase.			
KW	Human; protein kinase; protein phosphatase; signal transduction;			
XX	Intracellular signalling pathway.			
OS	Homo sapiens.			
PN	MO200109345-A1.			
PD	08-FEB-2001.			
PF	28-JUL-2000; 2000MO-JP05060.			
XX	29-JUL-1999; 99JP-0248036.			
PR	18-OCT-1999; 99OS-0159590.			
PR	11-JAN-2000; 2000JP-0118776.			
PR	17-FEB-2000; 2000US-0183322.			
PR	02-MAY-2000; 2000JP-0183767.			
PA	(HELIX-) HELIX RES INST.			
PI	Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;			
PI	Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;			
PI	Senoo C, Nezu J;			
DR	WPI: 2001-564736/63.			
DR	N-PDB: AAH78068.			
PT	New genes encoding protein kinase and protein phosphatase, useful for			
PT	identifying modulators which can be used to treat human or animal			
PS	disorders associated with the expression or function of these enzymes			
CC	Claim 2: Page 125-128; 336pp; Japanese.			
CC	The present sequence represents a human protein kinase/protein			
CC	phosphatase. The polypeptides are expected to participate in signal			
CC	transduction in cells. The kinase phosphatases are connected with			
CC	intracellular signalling pathways. Antisense oligonucleotides and			
CC	compounds identified by screening (agonists or antagonists) can be			
CC	used to treat human or animal disorders associated with the expression			
CC	or function of the protein. In addition, the polypeptides may be used			
CC	as target molecules fir drug development.			
Sequence	454 AA.			
Query Match	83.2%; Score 1117; DB 22; Length 454;			
Best Local Similarity	79.5%; Pred. No. 1.2e-104;			

Matches 209; Conservative 36; Mismatches 18; Indels 0; Gaps 0;

QY 1 YDIGEELSGQFAIVKCKREKSTGLEIAAKFIKKRQSRASRGVSREIREVSIKQVL 60
 13 yemgeelsgqfaivrcqkqgltgkeyaakfikkrrlssrrgvsreelerevsiileir 72

QY 61 HHNVITLHDVYKERTDVVHLELVSGELDFDLAOKESLSEEFATSPRIKQILGQVNLHT 120
 73 hpnlltldvfenktcdvlllelvsggellfllaekeslledaetqfllkqlldgvyhls 132

QY 121 KKAHFDLKPENIMLDDKNIPPIPIKILDFGLAHEIEDGVGFKNIFGTPPEFVAPAEIYNYE 180
 133 krlahfdlkipenimlldknpvprlklidfglahkieagsefknlfgtpetvapeivnye 192

QY 181 PLGLEADMSIGVITTYLLSGASPLGDTKQETLANITSVSYDFDEEFHSHTSELAKDFT 240
 193 plgleadmsigvityllsgaspligetkqetltnisavnydfdeeyfantselakdftl 252

QY 241 RKLIVKTRKRLTIOEALRHPWI 263
 253 rllivkdpkrrmtlaqslshswl 275

RESULT 7

AAV06922
 ID AAV06922 standard; Protein; 448 AA.

AC AAV06922;
 DT 01-JUL-1999 (first entry)
 DE Murine ZIP-kinase (serine/threonine kinase).
 KM ZIPper Interacting Protein Kinase; ZIP-kinase; serine/threonine kinase;
 KW leucine zipper domain; transcription factor ATF4; gene therapy; cancer;
 XX human; murine.
 OS Mus musculus.
 PN EP911408-A2.
 PD 28-APR-1999.
 PF 24-SEP-1998; 98EP-0307747.
 PR 26-SEP-1997; 97JP-0261589.
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 PI Akira S. Kawai T;
 DR WPI; 1999-246420/21.
 DR N-PSDB; AAK34657.
 PT New Recombinant Zipper Interacting Protein Kinase (ZIP-kinase)
 PT protein and DNA, useful as anticancer agents
 PS Claim 2; Page 19-22; 33pp; English.
 CC The invention provides human and murine recombinant zipper interacting
 CC protein kinase (ZIP-kinase) proteins. These proteins are serine/threonine
 CC kinases which bind the leucine zipper domain of transcription factor
 CC ATF4. Host cells containing vectors comprising the ZIP-kinase nucleic
 CC acids are used for the recombinant expression of the proteins. ZIP-kinase
 CC protein and DNA are useful as gene therapeutic agents against cancer, and
 CC as anti-cancer agents. The present sequence represents a murine ZIP
 CC kinase protein.
 SO Sequence 448 AA;

Query Match 82.4%; Score 1106; DB 20; Length 448;
 Best local Similarity 79.5%; Pred. No. 1,6e-103;

Matches 209; Conservative 34; Mismatches 20; Indels 0; Gaps 0;

QY 1 YDIGEELSGQFAIVKCKREKSTGLEIAAKFIKKRQSRASRGVSREIREVSIKQVL 60
 13 yemgeelsgqfaivrcqkqgltgkeyaakfikkrrlssrrgvsreelerevsiileir 72

QY 61 HHNVITLHDVYKERTDVVHLELVSGELDFDLAOKESLSEEFATSPRIKQILGQVNLHT 120
 73 hpnlltldvfenktcdvlllelvsggellfllaekeslledaetqfllkqlldgvyhls 132

QY 121 KKAHFDLKPENIMLDDKNIPPIPIKILDFGLAHEIEDGVGFKNIFGTPPEFVAPAEIYNYE 180
 133 krlahfdlkipenimlldknpvprlklidfglahkieagsefknlfgtpetvapeivnye 192

QY 181 PLGLEADMSIGVITTYLLSGASPLGDTKQETLANITSVSYDFDEEFHSHTSELAKDFT 240
 193 plgleadmsigvityllsgaspligetkqetltnisavnydfdeeyfantselakdftl 252

QY 241 RKLIVKTRKRLTIOEALRHPWI 263
 253 rllivkdpkrrmtlaqslshswl 275

RESULT 8

AA74205
 ID AA74205 standard; Protein; 1423 AA.

AC AA74205;
 DT 04-JAN-1980 (first entry)
 DE Human death associated protein DAP-2.
 KM Death associated protein; DAP; cytokine; cell death.
 KW Homo sapiens.
 OS Homo sapiens.
 FH Key
 FT Domain
 FT 13..267
 FT /label= protein kinase domain
 FT 280..312
 FT /label= calmodulin regulatory region
 FT 365..629
 FT /label= ankyrin repeats domain
 FT 365..397
 FT /label= ar1
 FT /note= "ankyrin repeat 1"
 FT 398..431
 FT /label= ar2
 FT 432..464
 FT /label= ar3
 FT 466..497
 FT /label= ar4
 FT 498..530
 FT /label= ar5
 FT 531..563
 FT /label= ar6
 FT 564..596
 FT /label= ar7
 FT 597..629
 FT /label= ar8
 FT 631..638
 FT /label= p-loop 1
 FT 587..594
 FT /label= p-loop 2
 PN WO9510630-A.
 PD 20-APR-1995.
 PF 12-OCT-1994; 94WO-US11598.
 PR 12-OCT-1993; 93IL-0107250.

PX	(RYCU/) RYCUS A.
PA	(YEDA) YEDA RES & DEV CO LTD.
PI	Klinchil A:
DR	WPI: 1995-178528/23.
N-P	N-PSSDB: AAQ69838, AAQ69839.
DNA	DNA whose expression mediates cytokine-induced programmed cell death - used to treat diseases or disorders associated with uncontrolled, pathological cell growth or cytokine-induced programmed cell death.
XN	Claim 8; Fig 8; 6lpp: English.
XX	DAP genes seem to play an imp. role in programmed cell death and the inhibition of their expression protects the cell from cytokine-promoted cell death. A cDNA library was generated from a mixture of mRNAs harvested after treatment of HeLa cells with IFN-gamma. It was cloned in antisense orientation into the EBV-based pTKO1 expression vector. The resulting expression library was introduced into HeLa cells. A fraction of the transfectants were selected with hygromycin B. The majority of transfected cells were infected by both hygrocytin B and IFN-gamma. The cells that survived and/or grew in the presence of IFN-gamma were expanded and pooled. The extrachromosomal DNA was obd., and cleaved with DpnI and introduced into E. coli HB101 host cells. A few bacterial clones were obt. which included DNA antisense sequences, some of which were able to protect cells from the death-promoting effects of IFN-gamma. PCR amplified DNAs inserts were generated from each plasmid using primers that corresp. to the immediate flanking sequence of the cDNA insertion sites in the pTKO1 vector. The PCR fragments were used as labeled probes to search Southern blots for possible cross hybridisation between some of the rescued antisense cDNA clones. The 10 cDNA clones were classified into six distinct non-overlapping gps., some constituting several members (clones) and some constituting a single member. Antisense cDNA clone 256 has the DNA product called DAP-2. Clone 256 (DAP-2) was sequenced and used to screen a K562 lambda gt10 cDNA library. The resulting composite sequence derived from 2 clones and the deduced AA sequence are shown in AAQ69838 and AAQ74205. The ORF is also shown in AAQ69839. CC CC AAQ69838 has a poly A tail. The calculated mol. wt. of the protein is about 160 kDa. Several known domains and motifs were identified in the protein (see AAQ74205 FT).
SQ	Sequence 1A23 AA;
Query Match	80.3%; Score 1079; DB 16; Length 1423;
Best Local Similarity	77.2% Pred. NO. 4.5e-100;
Matches 203; Conservative	39; Mismatches 13; Indels 8; Gaps 1.
Oy	1 VOIGELSGGGAFAIVKCKREKSTGLEVAKEITKRQRASRRGVSRERIEEVSILRQLV 60 : : : : : :
Bb	13 ydggeelsgqdfavvkckreksctglqpakflkrttsrrgsrfdleevsilkejd 72 : : : : : :
Oy	61 HHNVITLADVENDVDNHIELVLGGGLPDLAKESLSSEETSPFKOLLDVNLYLT 120 : : : : : :
Bb	73 hrvvltcheyenktvdllllelvaggelfdlakeesilleateeflkqlnglyylhs 132 : : : : : :
Oy	121 KKTAHPDKRENMLLRKNIPRIKLIDFGLAHIEDGVFERFNKTGPPEVADPYNYE 180 : : : : : :
Bb	133 lqtahfklkenlmldrnvrpkrlkidf-----gnetknlfgtpefvapelynye 184 : : : : : :
Oy	181 PLGLEADMWSIGVTYYLLS GASPFISGDTRKETLANITSVSVPDPDEFPSHTSELAKDFI 240 : : : : : :
Bb	185 plgleadmwsigvttyllssgaasplfgdtqcelanvasamvefedeyfnstsalakftfi 244 : : : : : :
Oy	241 RKLVVEKKRLTIOEARHPWI 263 : : : : : :
Bb	245 trllvwkdprkimtlgdsalqhpwi 267 : : : : : :

Query Match	80.3%;	Score 1079;	DB 19;	Length 1423;
Best Local Similarity	77.2%;	Pred. No. 4.5e-100;		
Matches 203;	Conservative 39;	Mismatches 13;	Indels	8; Gaps
1 YDIGELSGGFAIYKCKREKSTGLEYAKFKIKKRSRSPRGVSRREIEREVSILROYL 60				
13 ydtgeelsgsgfayavkckreksctgldypakfkikrrtktsrrrgsredieravallkeld 72				
61 HHNVITLHDVYERNDYVHILEVSGGELFDFLAOKESLSEDEATSPFKOLIDVNVNLT 120				
73 hpnvltlheyektdvllllevagsgelfdflaekeslteeaeflkqlingvyyllhs 132				
121 KTIADHDLKRENTMLDKNIPPHIKLIDFGLAHEIEGQVEKKNIFGTPREFAEIVNYE 180				
133 lqtlahfklpkenmllldrvpkrllidf-----gnetknlfygpelvapeivnye 184				
181 PLGEADMMWSIGVITVILLSGASPLGDTKQETLANITTSVSDIPDEEFPSHLSLAKDFI 240				

[illegible]

chronic inflammatory pelvic disease, multiple sclerosis, CC

8
9
10
11
12

CC The present sequence is a novel H

and the nucleic acids that encode them may be used in the

Query Match	47.28;	Score 634;	DB 22;	Length 372;
Best Local Similarly	48.38;	Pred. No. 9.1e-56;		
Matches 128;	Conservative 49;	Mismatches 74;	Indels 14;	Gaps 6;

0y 61 HHNVITLADVEYENRTDVHILELVSGEHLDFPLAQ--ESLSSEEAATSFQKILDGVNVL 118
I |||::|||::: || |::|::: : |::| : ||||::|::|
Db 92 h-vlnlheyenatcel|vleyaagaelfnclcpelaemvsendvir|kqlqeghy| 149

OY 119 HTKIAHFDLKPENIMLLDKNPIPHKLIDFGLAHEIEGVFEFNIEGTDEFAVPEIYN 178
| | | ||||:| | : |::|||: : | : | ||||:||||:
Db 150 hqnnlvhd|kpgnt-llsslyplgd|kvdfmsr|xqnaseldelmqtveylaeeln 208

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OY      179 YEPGLGLEADMMSIGVITYILLSGASPFGLDTKQETLANITTSVSYPDEEFSHTSEIAKD 238
       1::   111::111::111::   111::   111::   111::   111::   111::
db      209 ydplctatdmwniqilaymltlhtspfyqednetylnsqvnydvsgemfssvsqiatld 268
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Qy      239 FIRKLVKETRKRLTIOEALRHPWI 263
         11:1111 111:111:
Db      269 f1as1lvknpekrptaesc1shsw1 293
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RESULT 14
ABB58144
ID ABB58144 standard; Protein; 7107 AA.

AC ABB58144;
XX
DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 1224.
XX
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical).

XX Drosophila melanogaster.
OS
XX
PN W0200171042-A2.

PD	27-SEP-2001.
XX	
PF	23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
BA (BEKE) DE CORR NY

AA Venter JC, Adams M, Li PWD, Myers EW,
PI
XX WPI; 2001-656860/75.
DR

DR N-PSDB; ABL02247.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX Disclosure: SEQ ID NO 1224; 21bp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from *Drosophila*. The invention
CC useful in developmental biology and in elucidating cell signaling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB161617-AB163511), expressed DNA
CC sequences (AB101840-AB161617) and the encoded proteins

CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

Query Match	Score	DB	Length
sq sequence /10/ AA;	46.78;	627.5;	22; 7107;

0v	1	YDGGELGSGGFIVKKCKREKSTGLEVAAKFKKROSRASRRGVSREERIEREVSILROYL	60				
		Rest Local Similarity	46.0%; Pred. NO. 2./e-53;				
		Matches	123; Conservatly	51; Mismatches	81; Indels	9; Gaps	3

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61 HNAVITTHNVYENPTDVHITLFIYSGGELFD-FLAOKESI SEEPATSEFIKQIILDGVNYLH 119
Db ydlleeigcgafigvvhrcrerstgnlfaakiflvshs-----vekdlirreidimqnlh 6191

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6192 hqkllnlhfafeddemillileflsggelferitaegyvmteaeavlnymrglceglrhh 6253
      | | | | : : : | : | | | : : : | : | | | : : : |
0v 120 tktatHEDI KQENIM I DKNTDIDYIKI IDGCI AHFTNGVVEKKECTSDPEVADETIVY 179

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0x      : | | | | | | | | :: ||||| | | | | | | | | | |
db 6252 eqn1hldlkenlmqtrs--stnwklldfglatridnevwklttctaefape1vnr 6309
180 FBICIEADWMSGTVTITII SCASDELCDTCEQETI ANITSVSCVDNEDEEESUMSLAKPE 239
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      ||| :||| ||| | :|| : : ||| | : |||
db 6310 epvgyftclmatgvisyvlslspfcagdnvqtlknkacddfavesfkylseandf 6369

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Db 6370 irklvrnkekrmthacilhpwl 6393
      |||||: ||:| | | |||:

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AAV27162	AAV27162 standard; Protein; 372 AA
ID	AAV27162 standard; Protein; 372 AA
XX	
AC	AAV27162.

AA	15-SEP-1999 (first entry)
DT	
XX	
DE	Human DRAK2 protein.

KW DRK1; DRK2; DAP kinase related apoptosis inducing kinase; human;
 KW apoptosis; breast cancer; ovarian cancer; lymphoma; autoimmune disease;
 KW viral infection; adenovirus; poxvirus; HIV; Alzheimer's disease;

KW	diabetes.
XX	
OS	Homo sapiens.
XX	

PN	WO9933961-A1.
XX	
PD	08-JUL-1999.
MM	

XX	25-DEC-1998;	98WO-JP05974.
PF		
XX		
PR	17-APR-1998:	98JP-0108150.

PR 26-DEC-1997; 97JP-0367640.
 PR 26-DEC-1997; 97JP-0367641.
 PR 17-APR-1998; 98JP-0108149.
 XX
 PA (ASAH) ASAH KASEI KOGYO KK.
 XX
 PI Akira S, Kawai T;
 XX WPI: 1999-430239/36.
 DR N-PSDB: AAX89198.
 XX
 PT New kinase with apoptosis induction activity useful in the treatment
 XX of cancer, autoimmune diseases and viral infections
 XX
 PS Claim 2: Page 141-144; 180pp; Japanese.
 XX
 CC The invention provides kinases DRAK1 and DRAK2 (DAP kinase related
 CC apoptosis inducing kinase) having apoptosis inducing activity. The
 CC kinases can be expressed recombinantly by transforming host cells with
 CC vectors comprising the nucleic acids encoding the kinases. The kinases
 CC are useful in the treatment, prevention, diagnosis and investigation of
 CC diseases with which apoptosis is associated, such as hormonally regulated
 CC cancer (such as breast cancer, ovarian cancer, lymphoma), autoimmune
 CC diseases; viral infections (such as herpes, adenovirus, poxvirus, HIV);
 CC Alzheimer's disease; Parkinson's disease; arteriosclerosis; alcoholism;
 CC Rheumatoid arthritis; and diabetes. The present sequence represents the
 CC human DRAK2 amino acid sequence.
 XX
 SQ Sequence 372 AA;

Query Match 46.5%; Score 625; DB 20; Length 372;
 Best Local Similarity 48.3%; Pred. No. 7.4e-55;
 Matches 127; Conservative 46; Mismatches 80; Indels 10; Gaps 5;

OY	5	EELSGGFALVKKCRKSTGLTAYAKTKKQSRASRGVS--REIEREVSILROYLH-H 62
DB	37	keltgrqkfavrvqclskstgqeyaaakflkr-----rrgdcracellhelavlelaksrp 91
OY	63	NVTLTDVYENRFDVHILELVSGELDFDLAQK--ESLSEBATSFTKQILDGVNYLHT 120
DB	92	rvinlhevyeutseililleyaaggelfelclpelaemvsendvrlrlkqllgvyylng 151
OY	121	KKIAHFDLKPENIMLLDKNIPRIKILIDFGLAHEIDGVEFKNIFGTPEFVAPRIYVE 180
DB	152	nnlvhldlkpgnl-llsslyplgdlkivdigmrkighacellreimgpeylapellnyd 210
OY	181	PLGLEADMSIGVTYLLSGASPFGLDTKQETLANITSVSYDFDEFFSHTSELAKDPI 240
DB	211	pitcatdmwnlgilaymlchitspfygndgetylnisgvndyseetlssvsqlatdfti 270
OY	241	RKLIVKETRRRLTQELRHPIW 263
DB	271	qslivknekrptaelclshswl 293

Search completed: May 18, 2002, 04:47:26
 Job time: 18480 sec